

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 01:45:57 ; Search time 183 Seconds

(without alignments)
64.360 Million cell updates/sec

Title: US-10-766-752b-5

Perfect score: 131

Sequence: 1 AGKPDGKRGDACEGDSGPFV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	146	2	Q6REN1
2	131	100.0	259	2	Q6REN1
3	131	100.0	295	2	Q6REN1
4	131	100.0	622	1	THRB_HUMAN
5	131	100.0	622	1	THRB_HUMAN
6	127	96.9	235	2	Q287J1
7	124	94.7	625	1	THRB_BOVIN
8	118	90.1	235	2	Q6REN1
9	118	90.1	524	2	Q6REN1
10	118	90.1	612	2	Q6REN1
11	113	86.3	235	2	Q6REN1
12	113	86.3	607	2	Q6REN1
13	113	86.3	607	2	Q6REN1
14	113	86.3	608	2	Q6REN1
15	113	86.3	615	2	Q6REN1
16	109	83.2	239	2	Q6REN1
17	105	80.2	420	2	Q6REN1
18	102	77.9	618	1	THRB_RAT
19	102	77.9	618	1	THRB_MOUSE
20	98	74.8	172	2	Q6REN1
21	92	70.2	234	2	Q6REN1
22	73.5	56.1	290	1	PR27_HUMAN
23	73.5	56.1	320	2	Q6REN1
24	73.5	56.1	721	2	Q6REN1
25	72.5	55.3	272	2	Q6REN1
26	72.5	55.3	389	2	Q6REN1
27	72.5	55.3	974	2	Q6REN1
28	71.5	54.6	417	1	HEPS_HUMAN
29	71.5	54.6	436	1	HEPS_MOUSE
30	71.5	54.6	799	2	Q6REN1
31	71.5	54.6	802	2	Q6REN1

32	71.5	54.6	811	1	TMS6_HUMAN
33	71.5	54.6	811	1	TMS6_MOUSE
34	71.5	54.6	824	2	Q6REN1
35	71.5	54.2	144	2	Q6REN1
36	71.5	54.2	144	2	Q6REN1
37	71.5	54.2	161	1	PR27_HUMAN
38	71.5	54.2	195	2	Q6REN1
39	71.5	54.2	195	2	Q6REN1
40	71.5	54.2	195	2	Q6REN1
41	71.5	54.2	195	2	Q6REN1
42	71.5	54.2	211	2	Q6REN1
43	71.5	54.2	461	1	PR27_HUMAN
44	70.5	53.8	161	2	Q6REN1
45	70.5	53.8	259	2	Q6REN1

ALIGNMENTS

RESULT 1	Q6REN1	PRELIMINARY	PRT	146 AA
AC	Q6REN1			
DT	05-JUL-2004 (TREMblrel. 27, Created)			
DT	05-JUL-2004 (TREMblrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMblrel. 27, Last annotation update)			
DE	Coagulation factor II (Fragment).			
OS	Sub scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_Taxid=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Tissue=Liver;			
RA	Scheffner I., Christ B.;			
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1 SIMILARITY: Belongs to peptidase family S1.			
DR	EMBL; AY098976; AAR9595.1; -.			
DR	HSP; P00734; 1BA8.			
DR	GO; GO:0004263; Fichymotrypsin activity; IEA.			
DR	GO; GO:0008233; Fipeptidase activity; IEA.			
DR	GO; GO:0004295; Fipeptidase activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro: IPR001254; Peptidase_S1.			
DR	InterPro: IPR001314; Peptidase_S1a.			
DR	InterPro: IPR009003; Pept_Ser_Cys.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00020; TRYSPC; 1.			
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00135; TRYPSIN_SRR; 1.			
KW	Hydrolase; Protease; Serine protease.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	146 AA; 16530 MW; 53636A1FB180A73 CRC64;		
Query Match		100.0%; Score 131; DB 2; Length 146;		
Best Local Similarity		100.0%; Pred. NO. 6.6e-10;		
Matches	23; Conservative	0; Mismatches	0; Indels	0;
QY	1 AGKPDGKRGDACEGDSGPFV 23			
DB	100 AGKPDGKRGDACEGDSGPFV 122			
RESULT 2	Q6REN1	PRELIMINARY	PRT	259 AA
AC	Q6REN1			
DT	25-OCT-2004 (TREMblrel. 28, Created)			
DT	25-OCT-2004 (TREMblrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMblrel. 28, Last annotation update)			
DE	Prothrombin B-chain (Fragment).			
OS	Homo sapiens (Human).			

Qy	Db	1	AGYKPEDEKRGADCGSGGPPV 23	188	AGYKPEDEKRGADCGSGGPPV 210
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
KN	(1)				
RP	SEQUENCE FROM N.A.				
RA	Gruber A., Hanson S.R., Dlicera E.;				
RT	"Antithrombotic Thrombin Variants."				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY344794; AAR08143.1; "				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.				
DR	GO; GO:0003809; F:thrombin activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0007596; P:blood coagulation; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001254; Peptidase_S1.				
DR	InterPro; IPR001314; Peptidase_S1A.				
DR	InterPro; IPR003966; Peptidase_S1A.pr.				
DR	InterPro; IPR009003; Pept_Ser_Cys.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	PRINTS; PR01505; PROTHROMBIN.				
DR	SMART; SMO0020; Tryp_Spec; 1.				
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE; PS00135; TRYPSIN_SER; 1.				
KW	Hydrolase; Protease; Serine protease.				
FT	NON TER				
SO	SEQUENCE 259 AA; 29565 MW; B8D4D220B5D9FDE8 CRC64;				
Query Match	100.0%; Score 131; DB 2; Length 259;				
Best Local Similarity	100.0%; Pred. No. 1.2e-09;				
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
KN	(1)				
RP	SEQUENCE FROM N.A.				
RA	Gruber A., Hanson S.R., Dlicera E.;				
RT	"Antithrombotic Thrombin Variants."				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY344794; AAR08142.1; "				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.				
DR	GO; GO:0003809; F:thrombin activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0007596; P:blood coagulation; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001254; Peptidase_S1.				
DR	InterPro; IPR001314; Peptidase_S1A.				
DR	InterPro; IPR003966; Peptidase_S1A.pr.				
DR	InterPro; IPR009003; Pept_Ser_Cys.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	PRINTS; PR01505; PROTHROMBIN.				
DR	SMART; SMO0020; Tryp_Spec; 1.				
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE; PS00135; TRYPSIN_SER; 1.				
KW	Hydrolase; Protease; Serine protease.				
FT	NON TER				
SO	SEQUENCE 259 AA; 29565 MW; B8D4D220B5D9FDE8 CRC64;				
Query Match	100.0%; Score 131; DB 2; Length 259;				
Best Local Similarity	100.0%; Pred. No. 1.2e-09;				
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
KN	(1)				
RP	SEQUENCE FROM N.A.				
RA	Gruber A., Hanson S.R., Dlicera E.;				
RT	"Antithrombotic Thrombin Variants."				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY344794; AAR08142.1; "				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.				
DR	GO; GO:0003809; F:thrombin activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0007596; P:blood coagulation; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; I				

DR PROSITE: PS00135; TRYPSIN_SER: 1.
KW Hydrolyase; Protease; Serine protease.

FT NON_TER 1
SQ SEQUENCE 295 AA; 33637 MW; 785321BC30738DE1 CRC64;

Query Match 100.0%; Score 131; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

ID	THRB_HUMAN	STANDARD	PRT	622 AA.
AC P00734;				
DT 21-JUL-1986 (Rel. 01, Created)				
DI -JAN-1990 (Rel. 13, Last sequence update)				
DT 25-OCT-2004 (Rel. 45, Last annotation update)				
DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).				
GN Name=P2;				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI_Taxid=9606;				
[1]				
PP SEQUENCE FROM N.A.				
RX MEDLINE=86077877; PubMed=2825773;				
RA Degen S.U.F., Davie E.W.;				
RL "Nucleotide sequence of the gene for human prothrombin.";				
Biochemistry 26:6165-6177(1987).				
[2]				
PP SEQUENCE FROM N.A. AND VARIANT MET-165.				
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,				
Ozuna M., Pool C.L., Toth E.O., Yi Q., Nickerson D.A.;				
"SeattlesPep. NHLBI HU66682 program for genomic applications, UW-				
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";				
Submitted (JAN-2002) to the EMBL/Genbank/DBD databases.				
[3]				
PP SEQUENCE OF 8-622 FROM N.A.				
RX MEDLINE=83231463; PubMed=6305407;				
RA Degen S.U.F., McGillivray R.T.A., Davie E.W.;				
RT "Characterization of the complementary deoxyribonucleic acid and gene				
coding for human prothrombin.";				
Biochemistry 22:2087-2097(1983).				
[4]				
PP SEQUENCE OF 44-314.				
RX MEDLINE=77193964; PubMed=266717;				
WAIZ D.A., Hewett-Emlert D., Seegers W.H.;				
RA "Amino acid sequence of human prothrombin fragments 1 and 2.";				
Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).				
[5]				
PP SEQUENCE OF 315-622.				
RX MEDLINE=77207112; PubMed=873923;				
BAUTKOWSKI R.U., ELTON J., DOWNING M.R., NAMM K.G.;				
RA "Primary structure of human prethrombin 2 and alpha-thrombin.";				
J. Biol. Chem. 252:4942-4957(1977).				
[6]				
PP PROCESSING.				
RX MEDLINE=87008532; PubMed=3759958;				
RA BODIE W., MAYR I., BAUNMAN U., HUBER R., STONE S.R., HOFSTEENGE J.;				
RT "The refined 1.9 Å crystal structure of human alpha-thrombin:				
interaction with D-Phe-Pro-Arg chromomethylketone and significance of				
the Tyr-Pro-Tyr insertion segment.";				
J. Biol. Chem. 261:13210-13215(1986).				
[7]				
PP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).				
RX MEDLINE=90059942; PubMed=2583108;				
RA RABIER M.J., BLANCHILL A., FURIE B., FURIE B.C.;				
RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin				
activation in human plasma.";				
J. Biol. Chem. 261:13210-13215(1986).				
[7]				

EMBO J. 8:3467-3475(1989).
 (8)
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=90327074; PubMed=2374926;
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Rolisch C., Fenton J.W. II;
 RT "The structure of a complex of recombinant hirudin and human alpha-
 RT thrombin.";
 RL Science 249:277-280(1990).
 (9)
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94350942; PubMed=8071320;
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin.";
 RL J. Biol. Chem. 269:22000-22006(1994).
 (10)
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=9757286; PubMed=9214615; DOI=10.1093/emboj/16.11.2977;
 RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
 RA Esmon C.T., Stubbs M.T.;
 RT "The thrombin E192Q-BPTI complex reveals gross structural
 RT rearrangements: Implications for the interaction with antithrombin and
 RT chromomodulin.";
 RL EMBO J. 16:2977-2984(1997).
 (11)
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
 RX MEDLINE=99162521; PubMed=10051558; DOI=10.1073/pnas.96.5.1852;
 RA Guinto E.R., Caccia S., Rose T., Fletterer K., Wakeman G., di Cera E.,
 RT "Unexpected crucial role of residue 225 in serine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 (12)
 RN VARIANT DYSPROTHROMBINEMIA CVS-314.
 RX MEDLINE=87033739; PubMed=3771562;
 RA Rabiet M.-O., Furler B.C., Furler B.;
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
 RT for arginine at residue 273.";
 RL J. Biol. Chem. 261:15045-15048(1986).
 (13)
 RN VARIANT DYSPROTHROMBINEMIA ALA-509.
 RX MEDLINE=95313001; PubMed=792730;
 RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
 RT substitution of Glu-466 by Ala.";
 RL Thromb. Haemost. 73:203-209(1995).
 (14)
 RN VARIANTS DYSPROTHROMBINEMIA THR-380 AND HIS-431.
 RX MEDLINE=93043342; PubMed=1421398;
 RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
 RA Yamaguchi K.;
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
 RT prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
 RL Blood 80:2275-2280(1992).
 (15)
 RN VARIANT DYSPROTHROMBINEMIA HIS-314.
 RX MEDLINE=95169898; PubMed=7865694;
 RA James H.L., Kim D.J., Zheng D.-Q., Gitolami A.;
 RT "Prothrombin Padua I: incomplete activation due to an amino acid
 RT substitution at a factor Xa cleavage site.";
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).
 (16)
 RN VARIANT DYSPROTHROMBINEMIA CVS-425.
 RX MEDLINE=89207504; PubMed=3242619;
 RA Heniksen R.A., Mann K.G.;
 RT "Identification of the primary structural defect in the dysfibrinogen
 RT chromogen Quick I: substitution of cysteine for arginine-382.";
 RL Biochemistry 27:9160-9165(1988).
 (17)
 RN VARIANT DYSPROTHROMBINEMIA VAL-601.
 RX MEDLINE=89247398; PubMed=2719946;
 RA Heniksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
 RT chromogen Quick II alters primary substrate specificity.";

Biochemistry 28:2078-2082(1989).
 (18)
 RN VARIANT DYSPROTHROMBINEMIA ALA-509.
 RX MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 RT reduces the fibrinogen clotting activity and the esterase activity.";
 RL Biochemistry 31:7457-7462(1992).
 (19)
 RN VARIANT DYSPROTHROMBINEMIA TRP-461.
 RX MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Imamoto T., Kawauchi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 RT that impairs the fibrinogen clotting activity of derived thrombin
 RT Tokushima.";
 RL Biochemistry 26:1117-1122(1987).
 (20)
 RN VARIANT DYSPROTHROMBINEMIA TRP-461.
 RX MEDLINE=87101511; PubMed=3801671;
 RA Imamoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 RT derived from a variant of human prothrombin.";
 RL Blood 69:565-569(1987).
 (21)
 RN VARIANT DYSPROTHROMBINEMIA TRP-461.
 RX MEDLINE=92256895; PubMed=1349838;
 RA Iwanaga H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 RT Tokushima. The application of PCR-SSCP for the genetic and molecular
 RT analysis of dysprothrombinemia.";
 RL Int. J. Hematol. 55:93-100(1992).
 (22)
 RN VARIANT DYSPROTHROMBINEMIA LYS-200.
 RX MEDLINE=83204687; PubMed=6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 RT type 3 (157 Glu leads to Lys) and the localization of a third thrombin
 RT cleavage site.";
 RL Br. J. Haematol. 54:245-254(1983).
 (23)
 RN VARIANTS MET-165 AND THR-386.
 RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardile K., Patel N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Zlaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 (24)
 RN ERRATUM.
 RX PubMed=10545957;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardile K., Patel N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Zlaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,
 RA Lander E.S.;
 RT "Nat. Genet. 23:373-373(1999).
 CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
 CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
 CC XI, and, in complex with thrombomodulin, protein C.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PM: The gamma-carboxyglutamate residues, which bind calcium ions,
 CC result from the carboxylation of glutamate residues by a microsomal

Query Match 100.0%; Score 131; DB 1; Length 622;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 551 AGYKPDGKRGDACEGDSGGPFV 573

RESULT 5
Q727P3 PRELIMINARY; PRT; 622 AA.

AC Q727P3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Coagulation factor II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bask S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalls D.E., Schmech A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051332; AAH51332.1; -.
DR HSSP; P00734; IHAG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidease_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00511; Kringl_1.
DR Pfam; PF00899; Trypsin_1.
DR ProDom; PD000395; Kringl_2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00130; KR_2.
DR SMART; SM00020; TYP_SPC_1.
DR PROSITE; PS00021; KRINGL_1; 1.
DR PROSITE; PS00021; KRINGL_1; 2.
DR PROSITE; PS00021; KRINGL_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Kringl_1; Protease; Serine protease.

SQ SEQUENCE 622 AA; 70008 MW; CA01E44024E0BE3F CRC64;

Query Match 100.0%; Score 131; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 551 AGYKPDGKRGDACEGDSGGPFV 573

RESULT 6
Q28731 PRELIMINARY; PRT; 235 AA.

AC Q28731;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Thrombin (Fragment).
GN Name=thrombin;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.A.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
DR EMBL; M81396; AAA31477.1; -.
DR PIR; C42696; C42696.
DR HSSP; P00734; IUVS.
DR MEROPS; S01.217; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidease_S1.
DR InterPro; IPR001314; Peptidease_S1A.
DR InterPro; IPR003966; Peptidease_S1A_pr.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR01505; PROTHROMBIN.
DR SMART; SM00020; TYP_SPC_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 235 AA; 27093 MW; 92FF3E4F93B360E0 CRC64;

Query Match 96.9%; Score 127; DB 2; Length 235;
Best Local Similarity 95.7%; Pred. No. 3.7e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 165 AGYKPDGKRGDACEGDSGGPFV 187

RESULT 7
THR3_BOVIN STANDARD; PRT; 625 AA.
ID THR3_BOVIN
AC P00735;
DT 21-JUL-1986 (Rel. 01, Created)

DT 01-APR-1990 (Rel. 14, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN Name: F2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88245190; PubMed=3379642;
 RA Irwin D.M., Robertson K.A., McGillivray R.T.A.;
 RT "Structure and evolution of the bovine prothrombin gene.";
 RL J. Mol. Biol. 200;31-45(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84203525; PubMed=6326805;
 RA McGillivray R.T.A., Davie E.W.;
 RT "Characterization of bovine prothrombin mRNA and its translation product.";
 RL Biochemistry 23:1626-1634(1984).
 RN [3]
 RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RA Magnusson S., Sottrup-Jensen L., Petersen T.E., Claess H.;
 RL (in) Hemker H.C., Veltkamp J.J. (eds.);
 RL Boehringer symposium on prothrombin and related coagulation factors,
 pp.25-46, Leiden University Press, Leiden (1975).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=86296631; PubMed=3741841;
 RA Park C.H., Tulinsky A.;
 RT "Three-dimensional structure of the kringle sequence: structure of
 prothrombin fragment 1.";
 RL Biochemistry 25:3977-3982(1986).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=9111686; PubMed=1856869;
 RA Sehnadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
 resolution.";
 RL J. Mol. Biol. 220:481-494(1991).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=92190185; PubMed=1547238;
 RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
 RT "The Ca²⁺ ion and membrane binding structure of the Gla domain of Ca-
 prothrombin fragment 1.";
 RL Biochemistry 31:2554-2566(1992).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92218459; PubMed=1560020;
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RT "The structure of residues 7-16 of the A alpha-chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92389219; PubMed=1518046;
 RA Brandeseder H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
 RA Martin P.D., Edwards B.F.P., Bode W.;
 RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
 formed with the benzamide and arginine-based thrombin inhibitors
 NAPPV, 4-TAPAP and WQPA. A starting point for improving
 antithrombotics.";
 RL J. Mol. Biol. 226:1085-1089(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
 RX MEDLINE=97102783; PubMed=8947023;
 RA van de Locht A., Stubbs W.T., Bode W., Friedrich T., Bollschweiler C.,
 RA Hoeffken W., Huber R.;
 RT "The ornithodorin-thrombin crystal structure, a key to the TAP
 enigma?";

RL EMBO J. 15:6011-6017(1996).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIBLIN.
 RX MEDLINE=98004486; PubMed=9342325; DOI=10.1073/pnas.94.22.11845;
 RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schlenning W.D.,
 RA Huber R., Bode W.;
 RT "Structure of the thrombin complex with triblin, a lipocalin-like
 exosite-binding inhibitor derived from a tritamine bug.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
 RN [11]
 RP GENE STRUCTURE.
 RX MEDLINE=86077733; PubMed=3000440;
 RA Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
 RT "Characterization of the bovine prothrombin gene.";
 RL Biochemistry 24:6854-6861(1985).
 CC [1-] FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
 CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
 CC XIII, and, in complex with thrombomodulin, protein C.
 CC [1-] CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC [1-] SUBCELLULAR LOCATION: Extracellular.
 CC [1-] TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC [1-] PTM: The gamma-carboxyglutamate residues, which bind calcium ions,
 CC result from the carboxylation of glutamate residues by a microsomal
 CC enzyme, the vitamin K-dependent carboxylase. The modified residues
 CC are necessary for the calcium-dependent interaction with a
 CC negatively charged phospholipid surface, which is essential for
 CC the conversion of prothrombin to thrombin.
 CC [1-] MISCELLANEOUS: Prothrombin is activated on the surface of a
 CC phospholipid membrane that binds the amino end of prothrombin and
 CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
 CC the activation peptide and cleaves the remaining part into light
 CC and heavy chains. The activation process starts slowly because
 CC factor V itself has to be activated by the initial, small amounts
 CC of thrombin.
 CC [1-] MISCELLANEOUS: Thrombin can itself cleave the amino terminal
 CC fragment (fragment 1) of the prothrombin, prior to its activation
 CC by factor Xa.
 CC [1-] SIMILARITY: Belongs to the peptidase S1 family.
 CC [1-] SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC [1-] SIMILARITY: Contains 2 kringle domains.
 CC [1-] DATABASE: NAME=Prozyme technical fact sheet;
 CC WWW="http://www.prozyme.com/technical/thrombindata.html".
 CC [1-] This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL, V00135; CAA23451.1; -.
 CC EMBL, J00041; AAA30781.1; -.
 CC PIR, S02537; TBRO.
 DR PDB, 1A0H; X-ray; N/D=208-366, B/E=367-625.
 DR PDB, 1AVG; X-ray; H=367-625, U=326-356.
 DR PDB, 1BBR; X-ray; E=517-625, H=367-516, U/L/M=318-366, K/N=367-625.
 DR PDB, 1ERJ; X-ray; H=367-625, L=318-366.
 DR PDB, 1ETS; X-ray; H=367-625, L=318-366.
 DR PDB, 1ERT; X-ray; H=367-625, L=318-366.
 DR PDB, 1HRT; X-ray; H=367-625, L=318-366.
 DR PDB, 1IDS; X-ray; H=367-622, L=318-366.
 DR PDB, 1MKW; X-ray; H/K/L=-.
 DR PDB, 1MXK; X-ray; H/K/L=-.
 DR PDB, 1NL2; X-ray; A=44-189.
 DR PDB, 1YBQ; X-ray; H/K=367-625, U/L=318-366.
 DR PDB, 1YBR; X-ray; H/K=367-625, U/L=318-366.
 DR PDB, 1YOC; X-ray; A/C/E/G=318-366, B/D/F/H=367-625.
 DR PDB, 1UCY; X-ray; E=517-625, H=367-516, U/L/M=318-366, K/N=367-625.
 DR PDB, 1UVT; X-ray; H=367-625, L=318-366.
 DR PDB, 1UVU; X-ray; H=367-625, L=318-366.

DR PDB; 1VIT; X-ray; F=367-516, G=517-625, H=367-625, L/M=318-366.
 DR PDB; 1YCP; X-ray; H=367-625, J/L=318-366, K=367-516, M=517-625.
 DR PDB; 2HPF; X-ray; P=214-292.
 DR PDB; 2PF2; X-ray; @=44-199.
 DR PDB; 2SPT; X-ray; @=44-199.
 DR PDB; 2SPT; X-ray; @=44-188.
 DR MEROS; S01.217; -.
 DR InterPro; IPR002383; GUA blood.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR009003; Pept Ser Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR003314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A.pr.
 DR InterPro; IPR00294; VitK_dep_GUA.
 DR Pfam; PF00594; GUA; 1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABROD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR PROSITE; PS00011; GUA 1; 1.
 DR PROSITE; PS00998; Kringle; 2.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR 3D-structure; Acute phase; Blood coagulation; Calcium-binding;
 DR Direct protein sequencing; Gamma-carboxyglutamic acid; Glycoprotein;
 DR Hydroxylase; Kringle; Plasma; Repeat; Serine protease; Signal;
 DR Vitamin K; Zymogen.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 43
 FT CHAIN 44 625 Prothrombin.
 FT PEPTIDE 44 199 Activation peptide (fragment 1).
 FT 200 317 Activation peptide (fragment 2).
 FT CHAIN 318 366 Thrombin light chain.
 FT CHAIN 367 625 Thrombin heavy chain.
 FT DOMAIN 44 90 GUA.
 FT DOMAIN 109 187 Kringle 1.
 FT DOMAIN 214 292 Kringle 2.
 FT SITE 367 625 Serine protease.
 FT SITE 199 200 Cleavage (by thrombin).
 FT SITE 317 318 Cleavage (by factor Xa).
 FT ACT_SITE 366 367 Cleavage (by factor Xa).
 FT ACT_SITE 409 409 Charge relay system.
 FT ACT_SITE 465 465 Charge relay system.
 FT ACT_SITE 571 571 Charge relay system.
 FT MOD_RES 50 50 4-carboxyglutamate.

Query Match 94.7%; Score 124; DB 1; Length 625;
 Best Local Similarity 95.7%; Pred. No. 2.6e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGKPDGKRGDACEGSGGPFV 23
 DB 554 AGKPDGKRGDACEGSGGPFV 576

RESULT 8
 Q090387 PRELIMINARY; PRT; 235 AA.
 AC 090387;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Thrombin (Fragment).
 GN Name=thrombin;
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.

OX NCBI_TaxID=8330;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., Macgillivray R.T.A.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).
 DR EMBL; M81395; AAA49391.1; -.
 DR PIR; F42696; F42696.
 DR HSSP; P00734; IUVS.
 DR MEROS; S01.217; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:trypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM0020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Protease; Serine protease.
 FT NON_TER 1 1
 SQ SEQUENCE 235 AA; 27272 MW; 49264DD9A57A41F CRC64;

Query Match 90.1%; Score 118; DB 2; Length 235;
 Best Local Similarity 91.3%; Pred. No. 6.1e-08;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGKPDGKRGDACEGSGGPFV 23
 DB 164 AGKPDGKRGDACEGSGGPFV 186

RESULT 9
 Q075X8 PRELIMINARY; PRT; 524 AA.
 AC 075X8;
 DT 01-OCT-2003 (TEMBLrel. 25, Created)
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Coagulation factor II (Thrombin).
 GN Name=f2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K.B., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomshiyki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Mulhally S.J.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hulton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-whole body;
 RA Strausberg R.;
 RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055596; AAH55596.1; -
 DR HSSP; P00734; 1B7X.
 DR ZFIN; ZDB-GENE-030131-4606; f2.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_Gla.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00069; Gla; 1.
 DR SMART; SM00020; TRYP_Spc; 1.
 DR PROSITE; PS00021; GLA_1; 1.
 DR PROSITE; PS50070; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR HydroLase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 524 AA; 59560 MW; 1BA4E0B11908025 CRC64;

Query Match 90.1%; Score 118; DB 2; Length 524;
 Best Local Similarity 87.0%; Pred. No. 1.4e-07;
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGYKPEDEKRGDACEGDSGSPV 23
 DB 449 AGYQPDPSKRGDACEGDSGSPV 471

RESULT 10

Q804W7 PRELIMINARY; PRT; 612 AA.
 ID Q804W7;
 AC Q804W7;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 RT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Prothrombin (EC 3.4.21.5).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OC NCB1_Taxid=31033;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lai K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF465278; AAC33373.1; -
 DR HSSP; P00734; 1UVS.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:trypsin activity; IEA.

DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007595; F:blood coagulation; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002383; Gla_blood.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_Gla.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00069; Gla; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRYP_Spc; 1.
 DR PROSITE; PS00021; GLA_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR HydroLase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 612 AA; 69622 MW; BA72DF3FDEB89BEAE CRC64;

Query Match 90.1%; Score 118; DB 2; Length 612;
 Best Local Similarity 87.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGYKPEDEKRGDACEGDSGSPV 23
 DB 544 AGYKPEDEKRGDACEGDSGSPV 566

RESULT 11

O91004 PRELIMINARY; PRT; 235 AA.
 ID O91004;
 AC O91004;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Thrombin (Fragment).
 GN Name=thrombin;
 OS Gecko gecko (Tokay gecko).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
 OC NCB1_Taxid=36310;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., MacGillivray R.T.A.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 DR EMBL; M81392; AAA49309.1; -
 DR PIR; E42696; E42696.
 DR HSSP; P00734; 1B7X.
 DR MEROPS; S01.217; -
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; F:blood coagulation; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.


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DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR01505; PROTHROMBIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Protease; Serine protease.
KM Hydrolyase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 235 AA; 26933 MW; 122A5C09F6F2276A CRC64;

Query Match 86.3%; Score 113; DB 2; Length 235;
Best Local Similarity 82.6%; Pred. No. 2,9e-07;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGSPFV 23
Db 164 AGYSPEDSKRGDACEGDSGSPFV 186

RESULT 12
ID Q91001 PRELIMINARY; PRT; 607 AA.
AC Q91001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Irwin D.M., Walz D.A., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94223694; PubMed=7513365;
RA Banfield D.K., Irwin D.M., Walz D.A., Macgillivray R.T.;
RT "Evolution of prothrombin: Isolation and characterization of the cDNAs
RT encoding chicken and haggfish prothrombin."
RL J. Mol. Evol. 38:177-187(1994).
DR EMBL; M81391; AAA21619.1; -.
DR PIR; DA2696; DA2696.
DR HSSP; P00734; IUVS.
DR MEROPS; S01.217; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00051; Kringle; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOD.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; TRYP_SPC; 1.

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DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Protease; Serine protease.
KM Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 607 AA; 69110 MW; 002F3606EA36270F CRC64;

Query Match 86.3%; Score 113; DB 2; Length 607;
Best Local Similarity 82.6%; Pred. No. 7,6e-07;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGSPFV 23
Db 537 AGYSPEDSKRGDACEGDSGSPFV 559

RESULT 13
ID Q6DFJ5 PRELIMINARY; PRT; 607 AA.
AC Q6DFJ5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Lpa-prov protein.
DE Lpa-prov protein.
GN Name=Lpa-prov; (African clawed frog).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenodromae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC076742; AAH76742.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.

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DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007566; F:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A.pr.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VILK_dep_GLA.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 607 AA; 69232 MW; A31911A36710A1E8 CRC64;

Query Match 86.3%; Score 113; DB 2; Length 607;
 Best Local Similarity 82.6%; Pred. No. 7.6e-07;
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKDEGRKGDACGDSGSPV 23
 DB 535 AGYSPDSKRGDAGSGSPV 557

RESULT 14
 Q9PTW7 PRELIMINARY; PRT; 608 AA.
 ID 09PTW7; AC 09PTW7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Prothrombin.
 GN Name=OSPT;
 OS Struthio camelus (Oestrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
 OC Struthio.
 QX NCBI_TaxID=8801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20579470; PubMed=1137455; DOI=10.1016/S1357-2725(00)00062-5;
 RA Frost C., Nade R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.,
 RT "Purification and characterization of ostrich prothrombin."
 RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
 DR EMBL; AB028871; BAA89046.1; -
 DR HSP; P00734; IUVS.
 DR MEROPS; S01.217; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007566; F:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A.pr.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VILK_dep_GLA.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 608 AA; 69392 MW; 11B974B9AEE54EA2 CRC64;

Query Match 86.3%; Score 113; DB 2; Length 608;
 Best Local Similarity 82.6%; Pred. No. 7.7e-07;
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKDEGRKGDACGDSGSPV 23
 DB 537 AGYSPDSKRGDAGSGSPV 559

RESULT 15
 Q6GNK4 PRELIMINARY; PRT; 615 AA.
 ID 06GNK4; AC 06GNK4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC43652 protein (Fragment).
 GN Name=LOC43652;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 QX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Meng X., Hsieh F.,
 RA Diatchenko L., Marulanda K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueiri T.B., Toshlyuk S., Carinici P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skalsky U., Small D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Warr M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

KN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391(2002).
KN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073504; AAH73504.1;
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0005509; F:calcium ion binding; IEA.
DR GO, GO:0004263; F:chymotrypsin activity; IEA.
DR GO, GO:0008233; F:peptidase activity; IEA.
DR GO, GO:0003809; F:thrombin activity; IEA.
DR GO, GO:0004295; F:trypsin activity; IEA.
DR GO, GO:0007596; F:blood coagulation; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro, IPR002383; GLA blood.
DR InterPro, IPR000001; Kringle.
DR InterPro, IPR001254; Peptidase_S1.
DR InterPro, IPR001314; Peptidase_S1A.
DR InterPro, IPR003966; Peptidase_S1A.pr.
DR InterPro, IPR009003; Pept_Ser_Cys.
DR InterPro, IPR000294; VitK_dep_GLA.
DR Pfam, PF00594; GLA; 1.
DR Pfam, PF00051; Kringle; 2.
DR Pfam, PF00089; Trypsin; 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR PRINTS, PR00001; GLABLOOD.
DR PRINTS, PR00018; KRINGLE.
DR PRINTS, PR01505; PROTHROMBIN.
DR ProDom, PD000395; Kringle; 2.
DR SMART, SM00069; GLA; 1.
DR SMART, SM00130; KR; 2.
DR SMART, SM00020; Tryp_Spc; 1.
DR PROSITE, PS00021; KRINGLE_1; 2.
DR PROSITE, PS00070; KRINGLE_2; 2.
DR PROSITE, PS02400; TRYPSIN_DOM; 1.
DR PROSITE, PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE, PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Kringle; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 615 AA; 70195 MW; 9063E380058336E1 CRC64;
Query Match 86.3%; Score 113; DB 2; Length 615;
Best Local Similarity 82.6%; Pred. No. 7,7e-07;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGYKPDGKRGKRDACEGDSGGPFV 23
|||::|||
DB 543 AGYSPEDSKRGDACEGDSGGPFV 565

Search completed: March 31, 2005, 01:55:59
Job time : 185 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 01:46:47 ; Search time 43 seconds

(without alignments)
51.465 Million cell updates/sec

Title: US-10-766-752b-5

Perfect score: 131
Sequence: 1 AGYKPEGRGADGACGDSGCPV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	622	1	TBRU
2	127	96.9	236	2	C42696
3	124	94.7	625	1	TBBO
4	118	90.1	234	2	D42696
5	113	86.3	235	2	D42696
6	113	86.3	235	2	I42696
7	110	84.0	236	2	I42696
8	109	83.2	239	2	G42696
9	102	77.9	617	2	S10511
10	102	77.9	618	2	A35827
11	89	67.9	235	2	H42696
12	71.5	54.6	417	1	S00845
13	71	54.2	461	1	KXRU
14	70.5	53.8	482	1	KXRU
15	70.5	53.8	638	1	KOHP
16	69.5	53.1	275	2	S40007
17	69.5	53.1	1524	2	T30337
18	68.5	52.3	161	2	I62744
19	68.5	52.3	488	1	EXHU
20	68.5	52.3	1019	2	A38738
21	67.5	51.5	161	2	I48158
22	67.5	51.5	282	2	I84621
23	67.5	51.5	459	2	J00419
24	67.5	51.5	475	1	EXCH
25	67.5	51.5	638	1	KQMSPL
26	67	51.1	225	2	S45356
27	66.5	50.8	309	2	B49878
28	66.5	50.8	1004	2	T30338
29	66.5	50.8	1004	2	T30338

30	65.5	50.0	267	2	S40006	trypsin (EC 3.4.21
31	65.5	50.0	274	2	S35339	trypsin (EC 3.4.21
32	65.5	50.0	275	2	S40005	trypsin (EC 3.4.21
33	65.5	50.0	277	2	S35340	trypsin (EC 3.4.21
34	65.5	50.0	638	1	KQRTPL	plasma kallikrein
35	64.5	49.2	237	2	S55378	serine proteinase
36	64.5	49.2	238	1	TRWVSY	trypsin-like prote
37	64	48.9	191	2	S54115	complement factor
38	64	48.9	246	1	DBHU	complement factor
39	64	48.9	456	1	KXBO	protein C (activat
40	64	48.9	2616	2	A57096	nudel protein prec
41	63.5	48.5	625	1	KFHU1	coagulation factor
42	63	48.1	461	1	JX0210	protein C (activat
43	62.5	47.7	375	1	A23689	limulus clotting e
44	62.5	47.7	416	1	S33777	hepsin (EC 3.4.21,
45	62.5	47.7	492	1	EXBO	coagulation factor

ALIGNMENTS

RESULT:1
TBRU
chrombin (EC 3.4.21.5) precursor [validated] - human
N:Alternate names: coagulation factor II
N:Contains: Prothrombin
C:Species: Homo sapiens (man)
C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 09-Jul-2004
C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
R:Degeen, S.J.F.; Davie, E.W.
Biochemistry 26, 6165-6177, 1987
A:Title: Nucleotide sequence of the gene for human prothrombin.
A:Reference number: A29351; MUID:8807877; PMID:2825773
A:Accession: A29351
A:Molecule type: DNA
A:Residues: 1-622 <DEG>
A:Cross-references: UNIPROT:P00734; GB:M17262; GB:M33691; NID:9558069; PIDD:AAC63054.1;
R:Degeen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 22, 2087-2097, 1983
A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
A:Reference number: A00914; MUID:83231469; PMID:6305407
A:Accession: A00914
A:Molecule type: mRNA
A:Residues: 8-163, 'N', 165-622 <DE2>
A:Cross-references: GB:V00595; GB:U00307; NID:937128; PIDD:CA23842.1; PIDD:91335344
A:Accession: B00914
A:Molecule type: DNA
A:Residues: 188-311 <DE3>
R:Walt, D.A.; Hewett-Evans, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A:Reference number: A37549; MUID:77193964; PMID:266717
A:Accession: A37549
A:Molecule type: Protein
A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,
R:Butkewicz, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.
J. Biol. Chem. 252, 4942-4957, 1977
A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
A:Reference number: A37550; MUID:77207112; PMID:873923
A:Accession: A37550
A:Molecule type: Protein
A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
R:Rabier, M.J.; Blahut, A.; Furie, B.; Furie, B.C.
J. Biol. Chem. 261, 13210-13215, 1986
A:Reference number: A37551; MUID:87008332; PMID:3759958
A:Contents: annotation; activation cleavages
R:MacGillivray, R.T.; Irwin, D.M.; Guinco, E.R.; Stone, J.C.
Ann. N. Y. Acad. Sci. 485, 73-79, 1986
A:Title: Recombinant genetic approaches to functional mapping of thrombin.
A:Reference number: I51952; MUID:87182874; PMID:3471151
A:Accession: I51952
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2, 'RI', 5-100 <RES>

```

A:Cross-references: GB:M33031; NID:g190723; PIDN:AA60220.1; PID:g190724
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C:Comment: can be removed either by factor Xa or thrombin, the cleavage into light and heavy chain
C:Comment: ser 314-Arg, are released in natural blood clotting.
C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
C:Comment: ent interaction with the negatively charged phospholipid membrane surface.
C:Genetics:
A:Gene: GDB:F2
A:Cross-references: GDB:119894; OMIM:176930
A:Map position: 11p11-11q12
A:Intons: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
F:1-24/Domains: signal sequence #status predicted <SIG>
F:25-43/Domains: propeptide #status predicted <PRO>
F:28-87/Domains: Gla domain homology <Gla>
F:44-622/Product: prothrombin #status experimental <MAT>
F:44-327/Domains: activation peptide #status experimental <APT>
F:108-186/Domains: kringe homology <KR1>
F:213-291/Domains: kringe homology <KR2>
F:328-363/Product: thrombin light chain #status experimental <LCH>
F:364-622/Product: thrombin heavy chain #status experimental <HCH>
F:364-613/Domains: trypsin homology <TRY>
F:45-50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:60-65,90-103,108-186,129-169,151-181,213-291,234-274,262-286/Dissulfide bonds: #status
F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:326-482,536-550,564-594/Dissulfide bonds: #status predicted
F:331-407/Dissulfide bonds: #status experimental
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carboxylate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental

Query Match 100.0%; Score 131; DB 1; Length 622;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGPFV 23
DB 551 AGYKPDGKRGDACEGDSGPFV 573

- RESULT 2
C42696
Chrombin (EC 3.4.21.5) B chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: C42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A>Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557283
A:Accession: C42696
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-236 <BAN>
A:Cross-references: UNIPROT:Q28731; GB:M81396
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-227/Domains: trypsin homology (fragment) <TRY>

Query Match 96.9%; Score 127; DB 2; Length 236;
Best Local Similarity 95.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGPFV 23
DB 165 AGYKPDGKRGDACEGDSGPFV 187

- RESULT 3
TBEO
Thrombin (EC 3.4.21.5) Precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: S02537; A00915; A37552; I46045; S67518
R:Irwin, D.M.; Robertson, K.A.; MacGillivray, R.T.A.
U. Mol. Biol. 200, 31-45, 1988
A>Title: Structure and evolution of the bovine prothrombin gene.
A:Reference number: S02537; MUID:88245190; PMID:3379642
A:Accession: S02537
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-625 <TRM>
A:Cross-references: UNIPROT:P00735
R:MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A>Title: Characterization of bovine prothrombin mRNA and its translation product.
A:Reference number: A00915; MUID:84203525; PMID:6326805
A:Accession: A00915
A:Molecule type: mRNA
A:Residues: 1-230, 'H', 232-625 <MAC>
A>Note: 600-Asn was also found
R:Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
in Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C., an
A:Reference number: A37552
A:Accession: A37552
A:Molecule type: protein
A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAG>
A>Note: the evidence for 231-Ser is strong
A>Note: disulfide bonds and carboxylate binding sites were determined
R:Park, C.H.; Tullinsky, A.
Biochemistry 25, 3977-3982, 1986
A>Title: Three-dimensional structure of the kringe sequence: structure of prothrombin I
A:Reference number: A37553; MUID:86296631; PMID:3741841
A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R:Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A>Title: Characterization of the bovine prothrombin gene.
A:Reference number: A37554; MUID:86077733; PMID:3000440
A:Contents: annotation; gene structure
R:MacGillivray, R.T.; Deegen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A>Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A:Reference number: I46045; MUID:81054926; PMID:6524059
A:Accession: I46045
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 466-599, 'N', 601-625 <MA2>
A:Cross-references: EMBL:V00135; NID:9772; PIDN:CA23451.1; PID:9808945
R:Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A>Title: Identification of the proteolytic thrombin fragments formed after cleavage with
A:Reference number: S67518; MUID:95154277; PMID:7851376
A:Accession: S67518
A:Status: preliminary
A:Molecule type: protein
A:Residues: 318-325,333-338, 'X', 340,367-374,481-484, 'X', 486-488,515-522 <PEJ>
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Thrombin is activated on the surface of a phospholipid membrane that binds
C:Comment: activation peptide and cleaves the remaining part into light and heavy chains. The activat
C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombin,
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
C:Comment: ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Superfamily: thrombin; Gla domain homology; kringe homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; glyc
F:1-24/Domains: signal sequence #status predicted <SIG>
F:25-43/Domains: propeptide #status predicted <PRO>
F:28-88/Domains: Gla domain homology <Gla>
F:44-625/Product: prothrombin #status experimental <MPT>
F:44-199/Domains: activation peptide 1 #status experimental <FRI>
F:109-187/Domains: kringe homology <KR1>

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F:200-317/Domain: activation peptide 2 #status experimental <FR2>
F:214-292/Domain: kringle homology <KR2>
F:318-366/Product: thrombin light chain #status experimental <LC1>
F:367-625/Product: thrombin heavy chain #status experimental <HC>
F:367-616/Domain: trypsin homology <TRY>
F:50-51,58-60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:61-66,91-104,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-553,5
F:120-144,419/binding site: carbohydrate (asn) (covalent) #status experimental
F:409,465,571/Active site: His, Asp, Ser #status experimental

Query Match 94.7%; Score 124; DB 1; Length 625;
Best Local Similarity 95.7%; Pred. No. 1.8e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDAGCGDSGSPV 23
DB 554 AGYKPDGKRGDAGCGDSGSPV 576

RESULT 4
F:2696
thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment)
C:Species: Cynops pyrogastor (fire-bellied newt)
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: F42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Note: sequence not
A:Accession: F42696
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-234 <BAN>
A:Cross-references: UNIPROT:Q90387; GB:M81395
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: hydrolase; serine proteinase

Query Match 90.1%; Score 118; DB 2; Length 234;
Best Local Similarity 91.3%; Pred. No. 4.9e-09;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDAGCGDSGSPV 23
DB 163 AGYKPDGKRGDAGCGDSGSPV 185

RESULT 5
F:2696
thrombin (EC 3.4.21.5) B chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: D42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: D42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <BAN>
A:Cross-references: UNIPROT:Q91001; GB:M81391
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 86.3%; Score 113; DB 2; Length 235;
Best Local Similarity 82.6%; Pred. No. 2.4e-08;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDAGCGDSGSPV 23
DB 164 AGYKPDGKRGDAGCGDSGSPV 186

RESULT 6
F:2696
thrombin (EC 3.4.21.5) B chain - tokay (fragment)
C:Species: Gekko gekko (tokay)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: F42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: F42696
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-235 <BAN>
A:Cross-references: UNIPROT:Q91004; GB:M81392
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 86.3%; Score 113; DB 2; Length 235;
Best Local Similarity 82.6%; Pred. No. 2.4e-08;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDAGCGDSGSPV 23
DB 164 AGYKPDGKRGDAGCGDSGSPV 186

RESULT 7
F:2696
thrombin (EC 3.4.21.5) B chain - Pacific hagfish (fragment)
C:Species: Eptacetus stouti (Pacific hagfish)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: I42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: I42696
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-236 <BAN>
A:Cross-references: UNIPROT:Q90504; GB:M81393
A:Note: nucleotide translation not given
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 84.0%; Score 110; DB 2; Length 236;
Best Local Similarity 82.6%; Pred. No. 6.3e-08;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDAGCGDSGSPV 23
DB 164 AGYKPDGKRGDAGCGDSGSPV 186

RESULT 8
F:2696
thrombin (EC 3.4.21.5) B chain - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: G42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: G42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <BAN>

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #ext_change 16-Aug-2004
 A/Accession: S00845
 R/Entry: S.P.; Loebe, K.R.; Hagen, F.S.; Kirsch, K.; Davie, E.W.
 A/Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain
 A/Reference number: S00845; MUID:88209431; PMID:2835076
 A/Accession: S00845
 A/Molecule type: mRNA
 A/Residues: 1-417 <LF>
 A/Cross-references: UNIPROT: P05961; EMBL: X07732; NID: g32063; PIDN: CAA30558.1; PID: g32064
 C/Genetics:
 A/Genes: GDB: HPN; TMRP31; hepsin
 A/Cross-references: GDB: 135685; OMIM: 142440
 A/Map position: 19q11-19q13.2
 C/Superfamily: trypsin homology
 C/Keywords: hydrolase; liver; serine proteinase; transmembrane protein
 F/23-45/Domain: transmembrane #status predicted <TM>
 F/163-400/Domain: trypsin homology <TRY>
 F/188-204,291-359,322-338,349-381/Diulfide bonds: #status predicted
 F/203,257,353/Active site: His, Asp, Ser #status predicted

Query Match 54.6%; Score 71.5; DB 1; Length 417;
 Best Local Similarity 69.6%; Pred. No. 0.024;
 Matches 16; Conservative 2; Mismatches 2; Indels 3; Gaps 2;

QY 1 AGYKDEGRKDGSGGPPV 23
 DB 339 AGI-PEGGI--DAGQDSGGPPV 358

RESULT 13
 KXHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 N/Alternate names: autoprothrombin IIA; plasma protein C
 C/Species: Homo sapiens (man)
 C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #ext_change 09-Jul-2004
 A/Accession: A22331; A25426; A21781; A23789; A00927
 R/Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A/Title: The nucleotide sequence of the gene for human protein C.
 A/Reference number: A22331; MUID: 85270390; PMID: 2991887
 A/Accession: A22331
 A/Molecule type: DNA
 A/Residues: 1-461 <POS1>
 A/Cross-references: UNIPROT: P04070; GB: M1128; NID: g19033; PIDN: AAA60166.1; PID: g190334
 R/Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A/Title: Evolution and organization of the human protein C gene.
 A/Reference number: A25426; MUID: 86120978; PMID: 3511471
 A/Accession: A25426
 A/Molecule type: DNA
 A/Residues: 1-445, 1-446-461 <PU>
 A/Cross-references: GB: M12712; NID: g190330; PIDN: AAA60165.1; PID: g190332
 R/Foster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A/Title: Characterization of a cDNA coding for human protein C.
 A/Reference number: A21781; MUID: 84272714; PMID: 6589623
 A/Accession: A21781
 A/Molecule type: mRNA
 A/Residues: 1-107, 461 <POS2>
 A/Cross-references: GB: X02059; NID: g190322; PIDN: AAA60164.1; PID: g190323
 R/Beckmann, R.J.; Schmidt, R.J.; Satterlee, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A/Title: The structure and evolution of a 461 amino acid human protein C precursor and 1
 A/Reference number: A23789; MUID: 85269639; PMID: 2991859
 A/Accession: A23789
 A/Molecule type: mRNA
 A/Residues: 1-461 <BRC>
 A/Cross-references: GB: X02750; NID: g35689; PIDN: CAA26528.1; PID: g763120
 R/Milletich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A/Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m

A/Reference number: A44605; MUID: 90293094; PMID: 1694179
 A/Contents: annotation; carbohydrate binding sites; activation peptide
 A/Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R/Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A/Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A/Reference number: A44606; MUID: 92184750; PMID: 1544894
 A/Accession: A44606
 A/Contents: annotation; beta-hydroxyaspartic acid
 C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 vation of factor Va is strongly enhanced by complexing with protein S. Protein C also f
 C/Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
 C/Genetics:
 A/Genes: GDB: PROC
 A/Cross-references: GDB: 120317; OMIM: 176860
 A/Map position: 2q13-2q21
 A/Intons: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/27-86/Domain: Gla domain homology <Gla>
 F/33-42/Domain: propeptide #status predicted <PRO>
 F/43-197/Product: protein C light chain #status predicted <LCH>
 F/92-131/Domain: EGF homology <EG1>
 F/140-175/Domain: EGF homology <EG2>
 F/200-461/Product: protein C heavy chain #status predicted <HCH>
 F/200-211/Domain: activation peptide #status predicted <APT>
 F/212-445/Domain: trypsin homology <TRY>
 F/48, 49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F/59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-171, 183-319, 238-254, 373-387, 398-426/D
 F/106-111/Diulfide bonds: #status predicted
 F/110/Binding site: carbohydrate (Thr) (covalent) #status absent
 F/113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F/139,290,335/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F/211-212/Cleavage site: Arg-Leu (thrombin) #status experimental
 F/253,299,402/Active site: His, Asp, Ser #status predicted
 F/371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 54.2%; Score 71; DB 1; Length 461;
 Best Local Similarity 81.2%; Pred. No. 0.031;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GKRGDACGDSGGPPV 23
 DB 392 GDRDPCGDSGGPPV 407

RESULT 14
 EXRT
 coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #ext_change 09-Jul-2004
 A/Accession: S49075; J04670; F50191; F50190; I62745
 R/Stanton, C.; Rose, R.P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A/Title: Evidence for competition between vitamin K-dependent clotting factors for intra
 A/Reference number: A58458; MUID: 96093366; PMID: 8578539
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA1>
 A/Cross-references: UNIPROT: O63207; EMBL: X79807; NID: g506600; PIDN: CAA56202.1; PID: g5066
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are show
 R/Stanton, C.; Rose, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A/Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; MUID: 96194815; PMID: 8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <STA2>
 A/Cross-references: EMBL: X79807; NID: g506600; PIDN: CAA56202.1; PID: g506601
 A/Experimental source: Cos-1 cell
 R/Enyoji, K.; Miyazaki, K.; Kato, H.


```
RESULT 2
US-08-330-594-8
; Sequence 8, Application US/08330594C
; Patent No. 6184342
; GENERAL INFORMATION:
; APPLICANT: CAREY, DARRELL H.
; APPLICANT: RAMAKRISHNAN, SHYAM
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
; FILE REFERENCE: CHBP:002
; CURRENT APPLICATION NUMBER: US/08/330,594C
; CURRENT FILING DATE: 1994-10-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-08-330-594-8

Query Match          100.0%; Score 131; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGYKPDGKRGDACEGDSGGPFV 23
DB      1 AGYKPDGKRGDACEGDSGGPFV 23

RESULT 3
US-09-644-038-8
; Sequence 8, Application US/09644038
; Patent No. 6602978
; GENERAL INFORMATION:
; APPLICANT: CAREY, DARRELL H.
; APPLICANT: RAMAKRISHNAN, SHYAM
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
; FILE REFERENCE: CHBP:002
; CURRENT APPLICATION NUMBER: US/09/644,038
; CURRENT FILING DATE: 2000-08-22
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: 08/330,594
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-644-038-8

Query Match          100.0%; Score 131; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGYKPDGKRGDACEGDSGGPFV 23
DB      1 AGYKPDGKRGDACEGDSGGPFV 23

RESULT 4
US-08-538-504-3
; Sequence 3, Application US/08538504
; Patent No. 6627731
; GENERAL INFORMATION:
; APPLICANT: CARNEY, DARRELL H.
; APPLICANT: GLENN, KEVIN C.
; TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES;
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,504
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSG:178/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-538-504-3

Query Match          100.0%; Score 131; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGYKPDGKRGDACEGDSGGPFV 23
DB      1 AGYKPDGKRGDACEGDSGGPFV 23

RESULT 5
US-09-909-348A-5
; Sequence 5, Application US/09909348A
; Patent No. 6815416
; GENERAL INFORMATION:
; APPLICANT: CARNEY, DARRELL H.
; APPLICANT: CROWTHER, ROGER S.
; APPLICANT: STERNBERG, JANET
; APPLICANT: BERGMANN, JOHN
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF
; TITLE OF INVENTION: THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR
; FILE REFERENCE: 303.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-09-909-348A-5

Query Match          100.0%; Score 131; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 01:47:33 ; Search time 43 Seconds
(without alignments)
39.929 Million cell updates/sec

Title: US-10-766-752B-5

Perfect score: 131

Sequence: 1 AGYKPDGKRGDACEGDSGSPFV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the chance being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	23	3	US-08-981-088-2
2	131	100.0	23	3	US-08-330-594-8
3	131	100.0	23	4	US-09-644-039-8
4	131	100.0	23	4	US-08-538-504-3
5	131	100.0	23	4	US-09-809-348A-5
6	131	100.0	23	4	US-09-909-348A-6
7	131	100.0	23	4	US-08-944-483-52
8	131	100.0	259	3	US-10-165-442-2
9	131	100.0	259	4	US-10-165-442-2
10	131	100.0	295	4	US-08-338-368-2
11	131	100.0	295	4	US-10-165-442-1
12	131	100.0	295	4	US-10-165-442-1
13	131	100.0	376	2	US-08-558-269-10
14	131	100.0	376	2	US-09-410-882-10
15	131	100.0	579	2	US-08-295-411-4
16	131	100.0	579	2	US-08-955-471-4
17	131	100.0	579	2	US-09-117-708-14
18	131	100.0	579	5	PCT-US92-10242-4
19	131	100.0	615	1	US-07-998-972A-3
20	131	100.0	615	1	US-08-463-953-3
21	131	100.0	615	1	US-08-463-953-3
22	131	100.0	615	5	PCT-US92-11357-3
23	131	100.0	622	3	US-08-952-967-8
24	131	100.0	622	4	US-09-054-272-42
25	127	96.9	42	1	US-08-293-778-11
26	122	93.1	23	4	US-09-631-137C-3
27	114	87.0	20	6	5352664-1

28	114	87.0	20	6	5352664-1	Patent No. 5352664
29	91	69.5	17	4	US-09-631-137C-5	Sequence 5, Appl
30	81	61.8	14	3	US-08-981-088-4	Sequence 4, Appl
31	81	61.8	15	3	US-08-981-088-3	Sequence 4, Appl
32	81	61.8	15	3	US-09-656-121-2	Sequence 2, Appl
33	81	61.8	15	4	US-09-656-121-3	Sequence 3, Appl
34	80	61.1	14	4	US-09-631-137C-7	Sequence 7, Appl
35	75	57.3	42	1	US-08-293-778-12	Sequence 12, Appl
36	75	57.3	42	1	US-08-293-778-14	Sequence 14, Appl
37	73.5	56.1	290	4	US-09-386-653A-9	Sequence 9, Appl
38	73.5	56.1	315	4	US-09-386-653A-9	Sequence 15, Appl
39	73	55.7	42	1	US-08-293-778-15	Sequence 25, Appl
40	71.5	54.6	164	3	US-09-518-046-25	Sequence 67, Appl
41	71.5	54.6	255	2	US-08-944-483-67	Sequence 3, Appl
42	71.5	54.6	256	2	US-09-027-337-3	Sequence 3, Appl
43	71.5	54.6	256	4	US-09-644-600-3	Sequence 3, Appl
44	71.5	54.6	256	4	US-09-654-600A-3	Sequence 2, Appl
45	71.5	54.6	376	4	US-09-820-002-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-981-088-2
Sequence 2, Application US/08981088

Patent No. 616824

GENERAL INFORMATION:

APPLICANT: BAR-SHAVIT, RACHEL

TITLE OF INVENTION: ANTI-METASTATIC AND ANTI-ANGIOGENIC

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSES: OLIVIER & BERRIDGE, PLC

STREET: P. O. BOX 19928

CITY: ALEXANDRIA

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,088

FILING DATE: 27-JAN-1998

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: OLIVIER, JAMES A

REGISTRATION NUMBER: 27,075

REFERENCE/DOCKET NUMBER: JMO 40455

TELEPHONE: (703)-836-6400

TELEFAX: (703)-836-2787

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-981-088-2

Query Match

Best Local Similarity 100.0%; Score 131; DB 3; Length 23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 AGYKPDGKRGDACEGDSGSPFV 23

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..320
; OTHER INFORMATION: /note="Prothrombin Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 321..579
; OTHER INFORMATION: /note="Prothrombin Heavy Chain"
US-08-295-411-4

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Query Match 100.0%; Score 131; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGYKPDGKRGDACEGDSGGPPV 23
Db 508 AGYKPDGKRGDACEGDSGGPPV 530

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Job time : 44 secs

RESULT 13
US-08-558-269-10
; Sequence 10, Application US/08558269
; Patent No. 5961973
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,269
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,800
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CRI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-558-269-10

Query Match 100.0%; Score 131; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 7.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPEGRGDACEGDSGSPFV 23
DB 305 AGYKPEGRGDACEGDSGSPFV 327

RESULT 14
US-09-410-882-10
; Sequence 10, Application US/09410882
; Patent No. 6287561
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,882

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,269
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: US 07/847,800
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CRI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-410-882-10

Query Match 100.0%; Score 131; DB 3; Length 376;
Best Local Similarity 100.0%; Pred. No. 7.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPEGRGDACEGDSGSPFV 23
DB 305 AGYKPEGRGDACEGDSGSPFV 327

RESULT 15
US-08-295-411-4
; Sequence 4, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSP1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids

CURRENT FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(259)
OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-4

Query Match 100.0%; Score 131; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGSPFV 23
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2b 188 AGYKPDGKRGDACEGDSGSPFV 210

RESULT 10
US-08-338-368-2
Sequence 2, Application US/0838368
Patent No. 6110721
GENERAL INFORMATION:
APPLICANT: GIBBS, CRAIG S.
APPLICANT: LEUNG, LAWRENCE L.K.
APPLICANT: TSIANG, MANUEL
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND COAGULATION
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: GILEAD SCIENCES, INC.
STREET: 353 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,368
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,038
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: HENSLEY, MAX D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 190.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-574-3000
TELEFAX: 415-573-4899
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-368-2

Query Match 100.0%; Score 131; DB 3; Length 295;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGSPFV 23
|||||

Db 224 AGYKPDGKRGDACEGDSGSPFV 246

RESULT 11
US-10-165-442-1
Sequence 1, Application US/10165442
Patent No. 6706512
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Antithrombotic Variant Thrombins
FILE REFERENCE: E056 1070.1
CURRENT APPLICATION NUMBER: US/10/165,442
CURRENT FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(36)
OTHER INFORMATION: Thrombin W215A A-Chain
FEATURE:
NAME/KEY: CHAIN
LOCATION: (37)..(295)
OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-1

Query Match 100.0%; Score 131; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGSPFV 23
|||||
Db 224 AGYKPDGKRGDACEGDSGSPFV 246

RESULT 12
US-10-165-442-3
Sequence 3, Application US/10165442
Patent No. 6706512
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Antithrombotic Variant Thrombins
FILE REFERENCE: E056 1070.1
CURRENT APPLICATION NUMBER: US/10/165,442
CURRENT FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(36)
OTHER INFORMATION: Thrombin WE A-Chain
FEATURE:
NAME/KEY: CHAIN
LOCATION: (37)..(295)
OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-3

Query Match 100.0%; Score 131; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGSPFV 23
|||||
Db 224 AGYKPDGKRGDACEGDSGSPFV 246

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
Db 1 AGYKPDGKRGDACEGDSGGPFV 23

RESULT 6

US-09-909-348A-6
; Sequence 6, Application US/09909348A
; Patent No. 6815416
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF
; TITLE OF INVENTION: THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: AMIDATION at C-terminus
; LOCATION: (23)...(23)
; OTHER INFORMATION: Valine is Amidated
US-09-909-348A-6

Query Match 100.0%; Score 131; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3, 8e-12;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
Db 1 AGYKPDGKRGDACEGDSGGPFV 23

RESULT 7

US-08-944-483-52
; Sequence 52, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/944,483
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 6183.US.01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 52:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 259 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6232456e
US-08-944-483-52

Query Match 100.0%; Score 131; DB 3; Length 259;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
Db 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 8

US-10-165-442-2
; Sequence 2, Application US/10165442
; Patent No. 6706512
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin w215A B-Chain
US-10-165-442-2

Query Match 100.0%; Score 131; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
Db 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 9

US-10-165-442-4
; Sequence 4, Application US/10165442
; Patent No. 6706512
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442

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OM protein - protein search, using sw model

Run on: March 31, 2005, 01:49:58 ; Search time 139 Seconds
(without alignments)
54.786 Million cell updates/sec

Title: US-10-766-752b-5

Perfect score: 131

Sequence: 1 AGYKDEGKRGDACEGSGGPFV 23

Scoring table:

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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	131	100.0	23	9	US-09-777-328-8
2	131	100.0	23	9	US-09-904-090-3
3	131	100.0	23	13	US-10-050-611-3
4	131	100.0	23	13	US-10-050-611-4
5	131	100.0	23	13	US-10-050-688-5
6	131	100.0	23	13	US-10-050-688-6
7	131	100.0	23	17	US-10-718-930-8
8	131	100.0	259	11	US-09-789-210-52
9	131	100.0	259	15	US-10-165-442-2
10	131	100.0	259	15	US-10-165-442-4
11	131	100.0	259	16	US-10-699-393-2
12	131	100.0	259	16	US-10-699-393-4
13	131	100.0	259	16	US-10-872-198-5

14	131	100.0	259	17	US-10-872-197A-5	Sequence 5, Appl1
15	131	100.0	295	15	US-10-165-442-1	Sequence 1, Appl1
16	131	100.0	295	15	US-10-165-442-3	Sequence 3, Appl1
17	131	100.0	295	16	US-10-699-393-1	Sequence 1, Appl1
18	131	100.0	295	16	US-10-699-393-3	Sequence 3, Appl1
19	131	100.0	622	14	US-10-020-141-8	Sequence 8, Appl1
20	131	100.0	622	14	US-10-017-631-2	Sequence 2, Appl1
21	131	100.0	622	14	US-10-214-992-116	Sequence 116, App
22	131	100.0	622	14	US-10-172-712-39	Sequence 29, App
23	131	100.0	622	16	US-10-872-198-149	Sequence 149, App
24	127	96.9	623	17	US-10-775-180-841	Sequence 841, App
25	124	94.7	250	10	US-09-898-837A-45	Sequence 45, Appl1
26	124	94.7	251	10	US-09-898-837A-41	Sequence 41, Appl1
27	122	93.1	23	13	US-10-050-692-6	Sequence 6, Appl1
28	121	92.4	25	9	US-09-909-348-5	Sequence 5, Appl1
29	121	92.4	25	9	US-09-909-122-5	Sequence 5, Appl1
30	121	92.4	25	13	US-10-050-692-5	Sequence 5, Appl1
31	81	61.8	15	16	US-10-756-774-2	Sequence 2, Appl1
32	81	61.8	15	16	US-10-756-774-3	Sequence 3, Appl1
33	75	57.3	13	17	US-10-843-299-14	Sequence 14, Appl1
34	73.5	56.1	254	15	US-10-094-749-2110	Sequence 2110, App
35	73.5	56.1	260	14	US-10-266-035-2	Sequence 2, Appl1
36	73.5	56.1	260	16	US-10-391-364-21	Sequence 21, Appl1
37	73.5	56.1	290	11	US-09-833-245-1294	Sequence 1294, App
38	73.5	56.1	290	13	US-10-040-655-7	Sequence 7, Appl1
39	73.5	56.1	290	13	US-10-041-006A-7	Sequence 7, Appl1
40	73.5	56.1	290	14	US-10-028-072-222	Sequence 222, App
41	73.5	56.1	290	14	US-10-140-808-222	Sequence 222, App
42	73.5	56.1	290	14	US-10-121-049-222	Sequence 222, App
43	73.5	56.1	290	14	US-10-123-994-222	Sequence 223, App
44	73.5	56.1	290	14	US-10-140-470-222	Sequence 223, App
45	73.5	56.1	290	14	US-10-175-746-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-09-777-328-8
Sequence 8, Application US/09777328
Patent No. US20020032314A1
GENERAL INFORMATION:
APPLICANT: CAREY, DARRELL H.
APPLICANT: RAMAKRISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHBP:002
CURRENT APPLICATION NUMBER: US/09/777.328
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 08/330,594
PRIOR FILING DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-777-328-8
Query Match 100.0%; Score 131; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0; Gaps 0;
Cy 1 AGYKDEGKRGDACEGSGGPFV 23
Db 1 AGYKDEGKRGDACEGSGGPFV 23
RESULT 2
US-09-904-090-3
Sequence 3, Application US/09904090

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; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/217,583
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-3
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Query Match          100.0%; Score 131; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AGYKPDGKRGDACEGDSGGPFV 23
Db      1 AGYKPDGKRGDACEGDSGGPFV 23
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RESULT 3
US-10-050-611-3
; Sequence 3, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3
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Query Match          100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 AGYKPDGKRGDACEGDSGGPFV 23
Db      1 AGYKPDGKRGDACEGDSGGPFV 23
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RESULT 4
US-10-050-611-4
; Sequence 4, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
```

```
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-terminal amidated fragment of human thrombin
; NAME/KEY: AMIDATION
; LOCATION: 23
; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4
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Query Match          100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AGYKPDGKRGDACEGDSGGPFV 23
Db      1 AGYKPDGKRGDACEGDSGGPFV 23
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RESULT 5
US-10-050-688-5
; Sequence 5, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-5
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Query Match          100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AGYKPDGKRGDACEGDSGGPFV 23
Db      1 AGYKPDGKRGDACEGDSGGPFV 23
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RESULT 6
US-10-050-688-6
; Sequence 6, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
```

```
/ APPLICANT: Stienberg, Janet
/ APPLICANT: Bergmann, John
/ TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
/ TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
/ TITLE OF INVENTION: RECEPTOR
/ FILE REFERENCE: 3033.1003-004
/ CURRENT APPLICATION NUMBER: US/10/050,688
/ CURRENT FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/909,348
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: 60/219,800
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 6
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide fragment of thrombin
/ NAME/KEY: AMIDATION
/ LOCATION: (23)...(23)
/ OTHER INFORMATION: CONH2
- US-10-050-688-6

Query Match          100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGSPV 23
Db 1 AGYKPDGKRGDACEGDSGSPV 23

RESULT 7
US-10-718-930-8
/ Sequence 8, Application US/10718930
/ Publication No. US20050019331A1
/ GENERAL INFORMATION:
/ APPLICANT: Carney, Darrell H.
/ APPLICANT: Ramakrishnan, Shyam
/ TITLE OF INVENTION: Synthetic Peptide Neutrophil Cell
/ TITLE OF INVENTION: Chemotactic Agents
/ FILE REFERENCE: 3033.1005-003
/ CURRENT APPLICATION NUMBER: US/10/718,930
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: US 09/777,328
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: US 08/330,594
/ PRIOR FILING DATE: 1994-10-28
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 8
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptide
US-10-718-930-8

Query Match          100.0%; Score 131; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGSPV 23
Db 1 AGYKPDGKRGDACEGDSGSPV 23

RESULT 8
US-09-789-210-52
/ Sequence 52, Application US/09789210
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/ Publication No. US20040241646A1
/ GENERAL INFORMATION:
/ APPLICANT: COHEN, MAURICE
/ COLPITTS, TRACEY L.
/ FRIEDMAN, PAULA N.
/ GRANADOS, EDWARD N.
/ KLASIS, MICHAEL R.
/ RUSSELL, JOHN C.
/ STEWART, KENT D.
/ STROUPE, STEVEN D.
/ TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
/ AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
/ OF THE PROSTATE
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Abbott Laboratories
/ STREET: 100 Abbott Park Road
/ CITY: Abbott Park
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/789,210
/ FILING DATE: 20-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/944,483
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6183.US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 259 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: None
/ SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-789-210-52

Query Match          100.0%; Score 131; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGSPV 23
Db 188 AGYKPDGKRGDACEGDSGSPV 210

RESULT 9
US-10-165-442-2
/ Sequence 2, Application US/10165442
/ Publication No. US20030215440A1
/ GENERAL INFORMATION:
/ APPLICANT: Emory University
/ TITLE OF INVENTION: Antithrombotic Variant Thrombins
/ FILE REFERENCE: E056 1070.1
/ CURRENT APPLICATION NUMBER: US/10/165,442
/ CURRENT FILING DATE: 2002-06-07
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 2
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LENGTH: 259
TYPE: PR
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(259)
OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-2

Query Match 100.0%; Score 131; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 10
US-10-165-442-4
Sequence 4, Application US/10165442
Publication No. US20030215440A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Antithrombotic Variant Thrombins
FILE REFERENCE: E056 1070.1
CURRENT APPLICATION NUMBER: US/10/165,442
CURRENT FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PR
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(259)
OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-4

Query Match 100.0%; Score 131; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 11
US-10-699-393-2
Sequence 2, Application US/10699393
Publication No. US20040120943A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Antithrombotic Variant Thrombins
FILE REFERENCE: E056 1070.1
CURRENT APPLICATION NUMBER: US/10/699,393
CURRENT FILING DATE: 2003-10-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 259
TYPE: PR
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(259)
OTHER INFORMATION: Thrombin W215A B-Chain
US-10-699-393-2

Query Match 100.0%; Score 131; DB 16; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 12
US-10-699-393-4
Sequence 4, Application US/10699393
Publication No. US20040120943A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Antithrombotic Variant Thrombins
FILE REFERENCE: E056 1070.1
CURRENT APPLICATION NUMBER: US/10/699,393
CURRENT FILING DATE: 2003-10-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PR
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
LOCATION: (1)..(259)
OTHER INFORMATION: Thrombin WE B-Chain
US-10-699-393-4

Query Match 100.0%; Score 131; DB 16; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGKRGDACEGDSGGPFV 23
DB 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 13
US-10-872-198-5
Sequence 5, Application US/10872198
Publication No. US2005002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andreas SCHREIDIG
APPLICANT: Christian VOETSMETER
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.0002U4
CURRENT APPLICATION NUMBER: US/10/872,198
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 259
TYPE: PR
ORGANISM: Homo sapiens
US-10-872-198-5

Query Match 100.0%; Score 131; DB 16; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGGPFV 23
|||
Db 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 14

US-10-872-197A-5
; Sequence 5, Application US/10872197A
; Publication No. US20050059126A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMEIER
; APPLICANT: Ulrich KETTLING
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U3
; CURRENT APPLICATION NUMBER: US/10/872,197A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-197A-5

Query Match 100.0%; Score 131; DB 17; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGGPFV 23
|||
Db 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 15

US-10-165-442-1
; Sequence 1, Application US/10165442
; Publication No. US20030215440A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(36)
; OTHER INFORMATION: Thrombin w215A A-Chain
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (37)..(295)
; OTHER INFORMATION: Thrombin w215A B-Chain
US-10-165-442-1

Query Match 100.0%; Score 131; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGGPFV 23
|||
Db 224 AGYKPDGKRGDACEGDSGGPFV 246

Search completed: March 31, 2005, 02:00:01
Job time : 140 secs

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